Amendments to the Specification:

Please replace the paragraph beginning at page 12, line 22 with the following amended paragraph:

Figure 14: Phage ELISAs for the display of a peptide fused to the C-terminus of protein VIII using an optimized linker sequence. A polyHis flag was fused to the C-terminus of protein VIII with intervening linkers as follows: (Gly) 8 (SEQ ID NO: 288) (open circles), (Gly)9 (SEQ ID NO: 289) (squares), (Gly)10 (SEQ ID NO: 290) (diamonds), (Gly) 12 (SEQ ID NO: 291) (triangles), or optimized linker-1 (filled circles). The highest levels of display were observed with the optimized linker. Phage were serially diluted 5-fold from a starting concentration of 10'3 phage/mL. An anti- (His) 5 (SEQ ID NO: 279) antibody (Qiagen) was used as the capture target.

Please replace the paragraph beginning at page 39, line 19 with the following amended paragraph:

The sequences of several known mature major coat proteins of filamentous bacteriophage aligned with the mature M 13 coat protein VIII (SEQ ID NO: 2) are shown in the Table below. Segments of the coat proteins were aligned with M 13 protein VIII so as to provide maximum identity with the M 13 protein without the introduction of any deletions or insertions. Numbering above the sequences refers to the residues of mature M 13 protein VIII. Protein sequences are taken from the Dayhoff protein database (accession numbers:M13, COAB_BPFD (SEQ ID NO: 2); Fl, COAB_BPFD (SEQ ID NO: 3); Fd, COAB_BPFD (SEQ ID NO: 4); Zj-2, COAB_BPZJ2 (SEQ ID NO: 5); If-1,COAT_BPIF1 (SEQ ID NO: 6);12-2, COAB_BPI22 (SEQ ID NO: 7); Ike, COAB_BPIKE (SEQ ID NO: 8)). Homologous residues are indicated with dashes. A sequence having a single deletion is also known (WO 92/18619). It can be seen that there is considerable homology among the sequences of these coat proteins, particularly among the M 13, fl, fd and Zj-2 coat proteins and among the If1, 122 and Ike coat proteins.

Please replace the paragraph beginning at page 41, line 22 with the following amended paragraph:

Preferred variants of M13, fl and fd coat protein VIII (SEQ ID NO: 2-4) contain at least one amino acid residue selected from the lists below in the position indicated:

Please replace the paragraph beginning at page 72, line 37 with the following amended paragraph:

Libraries were also constructed to vary the linker between the fused protein and protein VIII. For hGH display, the oligonucleotide Lstop was used to introduce two consecutive TGA stop codons within the linker between hGH and protein VIII. The resulting phagemid was used as template in a second round of the Kunkel method with a degenerate oligonucleotide (ZF) designed to introduce a linker of the form (Gly) 3 (Xaa) i4 (Gly) 2 (where Xaa is a variable position) (SEQ ID NO: 292) in place of the Gly/Ser-rich linker encoded by pS349. For SAV display, the linker was varied between SAV and variant protein VIII (Ie) (see Figure 2, for the sequence of protein VIII (le)). The oligonucleotide Lstop2 was used to introduce three consecutive TAA stop codons within the linker between SAV and protein VIII (1 e). The resulting phagemid was used as template for the production of libraries with linkers of variable length and sequence. The oligonucleotides LV5, LV10, LVI S> LY20, and LV25 were used to construct libraries with linkers containing 5, 10, 15, 20, or 25 variable residues, respectively.

Please replace the paragraph beginning at page 81, line 3 with the following amended paragraph:

Phage from the library were cycled through rounds of binding selection with an anti-(His) 4 antibody (Qiagen) as the capture target. After three or four rounds of selection, individual clones were assayed for hexaHis flag display using a phage ELISA with either the anti- (His) 4 (SEQ ID NO: 293) antibody or bovine serum albumin (BSA) as target. Of 72 clones assayed, six exhibited at least a two-fold greater signal when captured with the anti-(His) 4 (SEQ ID NO: 293) antibody rather than with BSA (Fig. 16). These clones were subjected to DNA sequence analysis and the protein sequence was deduced from the DNA sequence.

Please replace the paragraph beginning at page 84, line 36 with the following amended paragraph:

Phage from the libraries were pooled together and cycled through binding selection with an anti-(His) 4 (SEQ ID NO: 293) antibody (Qiagen) as the capture target. After two rounds of selection, individual clones were assayed for hexaHis flag display using a phage ELISA with the

anti-(His) 4 antibody as target. Three clones exhibiting strong signals were subjected to DNA sequence analysis and the selected linker sequences are shown below.

Please insert the sequence listing after the abstract.